

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO700 [herein designated as UNQ364 (DNA46776-1284)] (SEQ ID NO:89) and the derived protein sequence for PRO700.

The entire nucleotide sequence of UNQ364 (DNA46776-1284) is shown in Figure 34 (SEQ ID NO:89). Clone UNQ364 (DNA46776-1284) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 33-35 and ending at the stop codon at nucleotide positions 1329-1331 (Figure 34). The predicted polypeptide precursor is 432 amino acids long (Figure 35). The full-length PRO700 protein shown in Figure 35 has an estimated molecular weight of about 47,629 daltons and a pI of about 5.90. Important regions of the amino acid sequence of PRO700 include the signal peptide, corresponding to amino acids from about 1 to 33, regions homologous to disulfide isomerase, corresponding to amino acids from about 82-99, 210-255, and 345-360, a tyrosine kinase phosphorylation site, corresponding to amino acids from about 143-151, and an endoplasmic reticulum targeting sequence, corresponding to amino acids from about 429-432. Clone UNQ364 (DNA46776-1284) has been deposited with ATCC and is assigned ATCC Deposit No. 209721.

EXAMPLE 16: Isolation of cDNA Clones Encoding Human PRO702

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36623. Based on the DNA36623 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO702.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer (36623.f1) 5'-CGCTGACTATGTTGCCAAGAGTGG-3' (SEQ ID NO:98)

reverse PCR primer (36623.r1) 5'-GATGATGGAGGCTCCATACCTCAG-3' (SEQ ID NO:99)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36623 sequence which had the following nucleotide sequence

hybridization probe (36623.p1)

5'-GTGTTCATTGGCGTGAATGACCTTGAAGGGAGGGACAGTACATGTTCCAC-3' (SEQ ID NO:100)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO702 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO702 [herein designated as UNQ366 (DNA50980-1286)] (SEQ ID NO:96) and the derived protein sequence for PRO702.

The entire nucleotide sequence of UNQ366 (DNA50980-1286) is shown in Figure 36 (SEQ ID NO:96).

Clone UNQ366 (DNA50980-1286) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 22-24 and ending at the stop codon at nucleotide positions 853-855 (Figure 36). The predicted polypeptide precursor is 277 amino acids long (Figure 37). The full-length PRO702 protein shown in Figure 37 has an estimated molecular weight of about 30,645 daltons and a pI of about 7.47. Analysis of the

full-length native PRO702 amino acid sequence evidences the presence of a putative signal peptide from about amino acid 1 to about amino acid 25, potential N-glycosylation sites from about amino acid 230 to about amino acid 233 and from about amino acid 258 to about amino acid 261 and a C-type lectin domain signature sequence from about amino acid 248 to about amino acid 270. Clone UNQ366 (DNA50980-1286) has been deposited with ATCC on March 31, 1998 and is assigned ATCC deposit no. 209717.

Analysis of the amino acid sequence of the full-length PRO702 polypeptide suggests that it possesses significant sequence similarity to the conglutinin protein, thereby indicating that PRO702 may be a novel conglutinin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO702 amino acid sequence and the following Dayhoff sequences, S32436, P_R75642, P_W18780, P_W18781, A53330, AC002528_1, HSPPA2IC0_1, CA21_HUMAN, CA14_HUMAN and A61262.

EXAMPLE 17: Isolation of cDNA Clones Encoding Human PRO703

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43047. Based on the DNA43047 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO703.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-GAGAGCCATGGGGCTCCACCTG-3' (SEQ ID NO:103)

reverse PCR primer 1 5'-GGAGAATGTGGCCACAAC-3' (SEQ ID NO:104)

reverse PCR primer 2 5'-GCCCTGGCACAGTGACTCCATAGACG-3' (SEQ ID NO:105)

reverse PCR primer 3 5'-ATCCACTTCAGCGGACAC-3' (SEQ ID NO:106)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40654 sequence which had the following nucleotide sequence

hybridization probe

5'-CCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACG-3'

(SEQ ID NO:107)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO703 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO703 [herein designated as UNQ367 (DNA50913-1287)] (SEQ ID NO:101) and the derived protein sequence for PRO703.

The entire nucleotide sequence of UNQ367 (DNA50913-1287) is shown in Figure 38 (SEQ ID NO:101). Clone UNQ367 (DNA50913-1287) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 115-117 and ending at the stop codon at nucleotide positions 2305-2307

(Figure 38). The predicted polypeptide precursor is 730 amino acids long (Figure 39). The full-length PRO703 protein shown in Figure 39 has an estimated molecular weight of about 78,644 daltons, and a pI of about: 7.65. Important regions of the PRO703 amino acid sequence include the signal peptide, a cAMP- and cGMP-dependent protein kinase phosphorylation site, a CUB domain protein motif, N-glycosylation sites and a putative AMP-binding domain signature. Clone UNQ367 (DNA50913-1287) has been deposited with ATCC and is assigned ATCC deposit no. 209716.

EXAMPLE 18: Isolation of cDNA Clones Encoding Human PRO705

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43437. Based on the DNA43437 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO705.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AAGCGTGACAGCGGGCACGTC-3' (SEQ ID NO:110)

reverse PCR primer 5'-TGCACAGTCTCTGCAGTGCCCAGG-3' (SEQ ID NO:111)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43437 sequence which had the following nucleotide sequence

hybridization probe (43437.p1)

5'-GAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCCTG-3' (SEQ ID NO:112)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO705 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO705 [herein designated as UNQ369 (DNA50914-1289)] (SEQ ID NO:108) and the derived protein sequence for PRO705.

The entire nucleotide sequence of UNQ369 (DNA50914-1289) is shown in Figure 40 (SEQ ID NO:108). Clone UNQ369 (DNA50914-1289) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 566-568 and ending at the stop codon at nucleotide positions 2231-2233 (Figure 40). The predicted polypeptide precursor is 555 amino acids long (Figure 41). The full-length PRO705 protein shown in Figure 41 has an estimated molecular weight of about 62,736 daltons and a pI of about 5.36. Analysis of the full-length PRO705 sequence as shown in Figure 41 evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 23, a eukaryotic DNA topoisomerase I active site from about amino acid 418 to about amino acid 436, and various regions that show homology to various glypican proteins from about amino acid 237 to about amino acid 279, about amino acid 421 to about amino acid 458, about amino acid 53 to about amino acid 74, about amino acid 466 to about amino acid 504, about amino acid 308 to about amino acid 355, about amino acid 104 to about amino acid 156 and about amino acid 379 to about amino acid 410. Clone UNQ369 (DNA50914-1289) has been deposited with ATCC on March 31, 1998 and is